SEQUENCE LISTING

<110> BASCH, Ross S. ZHANG, Xin-Min

<120> PROTEIN THAT MODULATES THE STABILITY OF TRANSCRIPTIONAL REGULATORY CO MPLEXES REGULATING NUCLEAR HORMONE RECEPTOR ACTIVITY, DNA ENCODING SAME, AND ANTIBODIES THERETO

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<150> 60/248,191
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gag g Glu G 1				_				_					_	_	_	607
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tgt a Cys I 2																847
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tta g Leu G																991
gga a Gly A																1039
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Leu Ser Leu Ile Asp Ala Val Met Pro Asp Val Val Gln Thr Arg Gln 85 90 95

Gln Ala Tyr Arg Asp Lys Leu Ala Gln Gln Ala Ala Ala Ala Ala 100 105 110

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Asn Thr Ala Asn Gly Glu Glu Asn Gly Ala His Thr Ile Ala Asn Asn 130 135 140

His Thr Asp Met Met Glu Val Asp Gly Asp Val Glu Ile Pro Pro Asn 145 150 155 160

Lys Ala Val Val Leu Arg Gly His Glu Ser Glu Val Phe Ile Cys Ala 165 170 175

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Ala Arg Ile Trp Asn Leu Ser Glu Asn Ser Thr Ser Gly Ser Thr Gln 195 200 205

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460

455

Cys Val His Ile Trp Asn Thr Gln Thr Gly Ala Leu Val His Ser Tyr 475 465 470 480 Arg Gly Thr Gly Gly Ile Phe Glu Val Cys Trp Asn Ala Ala Gly Asp Lys Val Gly Ala Ser Ala Ser Asp Gly Ser Val Cys Val Leu Asp Leu 505 Arg Lys <210> 3 <211> 2078 <212> DNA Homo sapiens <213> <220> <221> CDS <222> (161)..(1705) <223> <400> 3 ccgggagggg ggagcggcgt tggaggccac cgtttccagc atcaacaaca gcaacttgtg 60 120 attggcggtg accggatatt cagttgcaca tccccacatc aatgcactgc caatgggtta 175 tatcctgtgt tgtgacctca tggtttaagt gggaataaag atg agt ata agc agt Met Ser Ile Ser Ser gat gag gtc aac ttc ttg gta tat aga tac ttg caa gag tca gga ttt 223 Asp Glu Val Asn Phe Leu Val Tyr Arg Tyr Leu Gln Glu Ser Gly Phe 15 271 tct cat tca gca ttt acc ttt ggt ata aaa agc cat atc agt cag tcc Ser His Ser Ala Phe Thr Phe Gly Ile Lys Ser His Ile Ser Gln Ser 30 319 aat ata aat ggt gcc ctc gtc cca ccc gct gca ttg att tct atc atc Asn Ile Asn Gly Ala Leu Val Pro Pro Ala Ala Leu Ile Ser Ile Ile 45 cag aaa ggt cta cag tat gta gaa gca gaa gtt agt att aat gag gat 367 Gln Lys Gly Leu Gln Tyr Val Glu Ala Glu Val Ser Ile Asn Glu Asp 55 60 415 ggt acc ttg ttt gat ggt cga cca ata gag tct ctg tcc ctg ata gat Gly Thr Leu Phe Asp Gly Arg Pro Ile Glu Ser Leu Ser Leu Ile Asp 70 75 463 gcc gta atg cct gat gta gta caa aca aga caa caa gct tat aga gat Ala Val Met Pro Asp Val Val Gln Thr Arg Gln Gln Ala Tyr Arg Asp 90 95 511 aag ett gea eag eaa eag gea get get get get gee gea get gea

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- Ile Cys Ile His Thr Leu Thr Lys His Gln Glu Pro Val Tyr Ser Val 435 440 445
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- Gln Val Leu Leu Asn Leu Gly Arg Ser Ile Cys Leu Tyr Thr Leu Pro 485 490 495
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gco Ala	c tcc a Ser	tgt Cys	tca Ser	ı gat Asp	gac Asp	: atç Met	g aca Thr	ttg Leu	aag Lys	g ato s Ile	tgg Trp	g agt Ser	ato Met	aaq Lys	g caa s Gln	1336

365	370	375	380
gat aac tgt gtc cat Asp Asn Cys Val His 385	gat ttg caa gca Asp Leu Gln Ala	cat aat aaa gaa att His Asn Lys Glu Ile 390	tat act 1384 Tyr Thr 395
att aag tgg agt cca Ile Lys Trp Ser Pro 400	aca gga cca ggg Thr Gly Pro Gly 405	aca aat aat cca aat Thr Asn Asn Pro Asn 410	gcc aac 1432 Ala Asn
ctt atg cta gca agt Leu Met Leu Ala Ser 415	gca tcc ttt gat Ala Ser Phe Asp 420	tct aca gtt agg tta Ser Thr Val Arg Leu 425	tgg gac 1480 Trp Asp
gta gac aga ggg att Val Asp Arg Gly Ile 430	tgc atc cat act Cys Ile His Thr 435	ttg aca aaa cat caa Leu Thr Lys His Gln 440	gag ccc 1528 Glu Pro
gtg tac agt gtg gct Val Tyr Ser Val Ala 445	ttt agt cct gat Phe Ser Pro Asp 450	ggc agg tat ctg gca Gly Arg Tyr Leu Ala 455	agt ggt 1576 Ser Gly 460
tct ttt gac aag tgt Ser Phe Asp Lys Cys 465	Val His Ile Trp	aac aca cag aca ggt Asn Thr Gln Thr Gly 470	gct cta 1624 Ala Leu 475
gtt cac agt tac agg Val His Ser Tyr Arg 480	g gga aca ggt gga g Gly Thr Gly Gly 485	att ttt gaa gtt tgc Ile Phe Glu Val Cys 490	tgg aac 1672 Trp Asn
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gtc tta gac ctt cgg Val Leu Asp Leu Arg 510	g aaa tag cgttacta g Lys	agt tggaagccat ggacco	gacta 1771
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His Ile Ser Gln Ser 35	r Asn Ile Asn Gly 40	Ala Leu Val Pro Pro 45	Ala Ala

Leu Ile Ser Ile Ile Gln Lys Gly Leu Gln Tyr Val Glu Ala Glu Val

	50					55					60				
Ser 65	Ile	Asn	Glu	Asp	Gly 70	Thr	Leu	Phe	Asp	Gly 75	Arg	Pro	Ile	Glu	Ser 80
Leu	Ser	Leu	Ile	Asp 85	Ala	Val	Met	Pro	Asp 90	Val	Val	Gln	Thr	Arg 95	Gln
Gln	Ala	Tyr	Arg 100	Asp	Lys	Leu	Ala	Gln 105	Gln	His	Ala	Ala	Ala 110	Ala	Ala
Ala	Ala	Ala 115	Ala	Ala	Thr	Asn	Gln 120	Gln	Gly	Ser	Ala	Lys 125	Asn	Gly	Glu
Asn	Thr 130	Ala	Asn	Gly	Glu	Glu 135	Asn	Gly	Ala	His	Thr 140	Ile	Ala	Asn	Asn
His 145	Thr	Asp	Met	Met	Glu 150	Val	Asp	Gly	Asp	Val 155	Glu	Ile	Pro	Ser	Asn 160
Lys	Ala	Val	Val	Leu 165	Arg	Gly	His	Glu	Ser 170	Glu	Val	Phe	Ile	Cys 175	Ala
Trp	Asn	Pro	Val 180	Ser	Asp	Leu	Leu	Val 185	Ser	Gly	Ser	Gly	Asp 190	Ser	Thr
Ala	Arg	Ile 195		Asn	Leu	Ser	Glu 200	Asn	Ser	Thr	Ser	Gly 205	Pro	Thr	Gln
Leu	Val 210	Leu	Arg	His	Cys	Ile 215		Glu	Gly	Gly	Gln 220	Asp	Val	Pro	Ser
Asn 225		Asp	Val	Thr	Ser 230				Asn		Glu	Gly	Thr	Leu	Leu 240
Ala	Thr	Gly	Ser	Tyr 245		Gly	Phe	Ala	Arg 250	, Il∈	: Trp	Thr	Lys	Asp 255	Gly
Asn	Leu	Ala	Ser 260		Leu	Gly	Gln	His 265	Lys	Gly	/ Pro	Ile	Phe 270	Ala	Leu

Lys Trp Asn Lys Lys Gly Asn Phe Ile Leu Ser Ala Gly Val Asp Lys

Thr Thr Ile Ile Trp Asp Ala His Thr Gly Glu Ala Lys Gln Gln Phe

275

290

Pro Phe His Ser Ala Pro Ala Leu Asp Val Asp Trp Gln Ser Asn Asn 310 315 Thr Phe Ala Ser Cys Ser Thr Asp Met Cys Ile His Val Cys Lys Leu Gly Gln Asp Arg Pro Ile Lys Thr Phe Gln Gly His Thr Asn Glu Val Asn Ala Ile Lys Trp Asp Pro Thr Gly Asn Leu Leu Ala Ser Cys Ser Asp Asp Met Thr Leu Lys Ile Trp Ser Met Lys Gln Asp Asn Cys Val His Asp Leu Gln Ala His Asn Lys Glu Ile Tyr Thr Ile Lys Trp Ser 385 390 395 Pro Thr Gly Pro Gly Thr Asn Asn Pro Asn Ala Asn Leu Met Leu Ala Ser Ala Ser Phe Asp Ser Thr Val Arg Leu Trp Asp Val Asp Arg Gly Ile Cys Ile His Thr Leu Thr Lys His Gln Glu Pro Val Tyr Ser Val 435 440 Ala Phe Ser Pro Asp Gly Arg Tyr Leu Ala Ser Gly Ser Phe Asp Lys 450 455 Cys Val His Ile Trp Asn Thr Gln Thr Gly Ala Leu Val His Ser Tyr 465

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